AMENDMENTS TO THE SPECIFICATION

Please replace the paragraph on page 22, lines 6 to 20, with the following amended paragraph:

In one aspect, the method further comprises expressing the variant nucleic acid to generate a variant phospholipase polypeptide. In alternative aspects, the modifications, additions or deletions are introduced by error-prone PCR, shuffling, oligonucleotide-directed mutagenesis, assembly PCR, sexual PCR mutagenesis, in vivo mutagenesis, cassette mutagenesis, recursive ensemble mutagenesis, exponential ensemble mutagenesis, site-specific mutagenesis, gene reassembly, Gene Site Saturation Mutagenesis™ (GSSM™) ~~gene site saturated mutagenesis (GSSM)~~, synthetic ligation reassembly (SLR) and/or a combination thereof. In alternative aspects, the modifications, additions or deletions are introduced by a method selected from the group consisting of recombination, recursive sequence recombination, phosphothioate-modified DNA mutagenesis, uracil-containing template mutagenesis, gapped duplex mutagenesis, point mismatch repair mutagenesis, repair-deficient host strain mutagenesis, chemical mutagenesis, radiogenic mutagenesis, deletion mutagenesis, restriction-selection mutagenesis, restriction-purification mutagenesis, artificial gene synthesis, ensemble mutagenesis, chimeric nucleic acid multimer creation and/or a combination thereof.

Please replace the paragraph on page 73, lines 17 to 33, with the following amended paragraph:

Any technique in molecular biology can be used, e.g., random PCR mutagenesis, see, e.g., Rice (1992) Proc. Natl. Acad. Sci. USA 89:5467-5471; or, combinatorial multiple cassette mutagenesis, see, e.g., Crameri (1995) Biotechniques 18:194-196. Alternatively, nucleic acids, e.g., genes, can be reassembled after random, or "stochastic," fragmentation, see, e.g., U.S. Patent Nos. 6,291,242; 6,287,862; 6,287,861; 5,955,358; 5,830,721; 5,824,514; 5,811,238; 5,605,793. In alternative aspects, modifications, additions or deletions are introduced by error-prone PCR, shuffling, oligonucleotide-directed mutagenesis, assembly PCR, sexual PCR mutagenesis, in vivo mutagenesis, cassette mutagenesis, recursive ensemble mutagenesis, exponential ensemble

mutagenesis, site-specific mutagenesis, gene reassembly, Gene Site Saturation Mutagenesis™ (GSSM™) ~~gene site saturated mutagenesis (GSSM)~~, synthetic ligation reassembly (SLR), recombination, recursive sequence recombination, phosphothioate-modified DNA mutagenesis, uracil-containing template mutagenesis, gapped duplex mutagenesis, point mismatch repair mutagenesis, repair-deficient host strain mutagenesis, chemical mutagenesis, radiogenic mutagenesis, deletion mutagenesis, restriction-selection mutagenesis, restriction-purification mutagenesis, artificial gene synthesis, ensemble mutagenesis, chimeric nucleic acid multimer creation, and/or a combination of these and other methods.

Please replace the paragraph on page 78, line 23 to page 79, line 2, with the following amended paragraph:

Saturation mutagenesis, or, GSSM™ ~~GSSM~~

In one aspect of the invention, non-stochastic gene modification, a "directed evolution process," is used to generate phospholipases with new or altered properties. Variations of this method have been termed "Gene Site Saturation Mutagenesis™ (GSSM™)," ~~"gene site saturation mutagenesis,"~~ "site-saturation mutagenesis," "saturation mutagenesis" or simply GSSM™. ~~"GSSM."~~ It can be used in combination with other mutagenization processes. See, e.g., U.S. Patent Nos. 6,171,820; 6,238,884. In one aspect, GSSM comprises providing a template polynucleotide and a plurality of oligonucleotides, wherein each oligonucleotide comprises a sequence homologous to the template polynucleotide, thereby targeting a specific sequence of the template polynucleotide, and a sequence that is a variant of the homologous gene; generating progeny polynucleotides comprising non-stochastic sequence variations by replicating the template polynucleotide with the oligonucleotides, thereby generating polynucleotides comprising homologous gene sequence variations.